In the Claims

Please amend the claims as follows. Applicants present a full set of claims showing markups of the claims with insertions and deletions indicated by underlining and strikethrough text, respectively.

1. (Currently amended) An isolated nucleic acid molecule selected from the group consisting of

(a) a nucleic acid molecule which comprises the nucleotide sequence set forth as SEQ ID NO:4 and which encodes SEQ ID NO:5,

(b) nucleic acid molecules that differ from the nucleic acid molecules of (a) in codon sequence due to the degeneracy of the genetic code, and

(c) full-length complete complements of (a) and (b).

2. (Previously presented) The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule consists of the nucleotide sequence of SEQ ID NO:4.

3. (Previously presented) The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises the coding region of the nucleotide sequence of SEQ ID NO:4.

4-6. (Canceled)

7. (Currently amended) An isolated nucleic acid molecule selected from the group consisting of:

(a) a fragment of nucleotides 1-993 of SEQ ID NO:4 consisting of contiguous nucleotides between 15 and 992 ~~nucleotides~~ in length, and

(b) full-length complements of "(a)", wherein the fragment excludes nucleic acid molecules which consist only of fragments of SEQ ID NO:8, and ~~wherein the fragment comprises at least~~ fragments of SEQ ID NO:8 having 5 or fewer contiguous nucleotides of SEQ ID NO:4 ~~that are not present in SEQ ID NO:8~~.

8-16. (Canceled)

17. (Previously presented) An expression vector comprising the isolated nucleic acid molecule of claim 1 operably linked to a promoter.

18. (Previously presented) An isolated host cell transformed or transfected with the expression vector of claim 17.

19. (Previously presented) The isolated host cell of claim 18, wherein the isolated host cell expresses an HLA molecule.

20-37. (Canceled)

38. (Currently amended) A method for diagnosing cancer, comprising:

contacting a biological sample isolated from a subject with a probe that hybridizes under high stringency hybridization conditions to SEQ ID NO:4, wherein the probe consists of the isolated nucleic acid molecule of claim 1 ~~or claim 7~~, wherein the high stringency hybridization conditions are hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrolidone, 0.02% Bovine Serum Albumin, 25mM NaH_2PO_4 (pH 7), 0.5% SDS, 2mM EDTA), wherein SSC is 0.15M sodium chloride/0.015M sodium citrate, pH 7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid and washing at 2 x SSC at room temperature and then at 0.1 x SSC/0.1 x SDS at 65°C, and

determining the binding of the probe to a nucleic acid molecule in the sample to determine expression of the nucleic acid molecule ~~in the sample~~, wherein the expression of the nucleic acid molecule is diagnostic for the presence of cancer in the subject.

39-57. (Canceled)

58. (Currently amended) A ~~The~~ method for diagnosing cancer ~~of claim 57, wherein the hybridization binding between the agent probe and the nucleic acid molecule is determined~~ comprising

detecting the presence of (a) SEQ ID NO:4, (b) a fragment of SEQ ID NO:4 consisting of between 22 and 992 contiguous nucleotides in length, wherein the fragment excludes nucleic acid molecules which consist only of fragments of SEQ ID NO:8, or (c) full-length complete complements of (a) or (b) by nucleic acid amplification.

59. (Previously presented) The method of claim 58, wherein the nucleic acid amplification is reverse transcribed polymerase chain reaction (RT-PCR).

60-61. (Canceled)